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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Busch M, Hain R;

(FARB) BAYER AG

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Phytoene synthase Phytoene synthase Nicotiana tabacum Nicotiana tabacum

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                         lc acid encoding tobacco zeta-carotene desaturase,
compounds with herbicidal activity
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transgenic plants
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          synthase coding sequence from N. tabacum
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Best Local Similarity 77.2%; Pred. No. 3.5e-237;
Matches 1187; Conservative 0; Mismatches 255;
                               ene synthase; transgenic plant; enhanced violet absorber; food colour; ss.
                                                                                                                                                                                                                                                                                            Grill LK,
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                                                                                      Location/Qualifiers
367..1599
/*tag= a
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Kumagai MH;
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                                     1538 GAACT - TCCTCTCCACTAGCAAAGACATGAATGAAGTAGTTGAGTCAATGAGTATTATAC 1596
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Pred. No. 1.7e-234;
0; Mismatches 274; Indels 107;
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                                                                                                                 1637 TATATTATTATTATACTGTTAAAAGGAAAGAATT 1674
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Kumagai MH;
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Best Local Similarity 76.4%;
Matches 1230; Conservative
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HELLMANN G M.
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                                                                                                                                                                                                                                                                                              Phytoene synthase; zeta carotene desaturase; herbicide; transgenic plant; plant growth regulator; herbicidal; tobacco; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s of
tabacum.
                                                                    ACTICACAAGGAGGCITAIGITAGCAAGCCAAAGAAGCITCICACCITGCCCAITGCIT 1510
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                                                                                                                                                                  GAAAAGTGACGGATAAATGGAGAAGCTTTATGAAGAAGCAAATCCAGAGGGCAAGAAAGT
                     TAACAGCGCTGCTGTTGTATCGCAAGATATTGGACGAGATTGAAGCCAACGACTACAACA
                                                 ATGCAAAATCTCTTGTGCCCCCTAATAGAACT - TCCTCTCCACTAGCAAAGACATGAATG
                                                                                                                             AAGTAGTTGAGTCAATG------AGTATTATACACTAAAGAAACTCAGGTACTTG
                                                                                                                                           TAAATGAGATATCTTTTGCTAAATGTGTATCATCAAAAGTAGATTGT-AAATTCAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences phytoene synthases and zeta-carotene desaturase from Nicotiana t
                                                                                                                                                                                              ACAATCTCTTGGTAGAATAT-TTTCTCCACACTCATCAAACCCTCAAGTGA 1727
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compounds with herbicidal activity -
                                                                                                                                                                                                                                                                                                                                                        synthase"
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333..1565
/*tag= a
/product= "phytoene s
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P-PSDB; AAM51842.
                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                    Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                           Busch M, Hain R;
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The sequences can be used to identify compounds capable of altering the expression of these genes, which are therefore useful as plant growth regulators and herbicides. They can also be used to produce transgenic plants. The present sequence is the coding sequence of a tobacco phytoene synthase.
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                                                                                                                                                                                                                                                     132 GIGGATATCTACAAGTATTGGTTTTTTGATAAAATAGGCTGAGGTGAGAAGGTAACATAA
                                                                                                                                                                                                                                                                                                                                                                                    GTCTGTTGCTTTGTTGTTGTTTTCTCCCACTTCCGAGGTCTCGAATGGGACAGGATT
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                                                                                                                                                  Score 857.8; DB 24; Length
Pred. No. 2.8e-234;
2; Mismatches 265; Indels
                                                                                                                Sequence 1712 BP; 540 A; 265 C; 421 G; 475 T; 11 other;
                                                                                                                                                  49.6%;
larity 76.7%;
Conservative
                                                                                                                                                                      Best Local Similarity
Matches 1206; Conserv
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95US-0579667

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27-DEC-1995;
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                                                                                                             GTTAACAGCGCTGCTGTTGTATCGCAAGATATTGGACGAGATTGAAGCCAACGACTACAA 1448
                                                                                                                                                                 CAACTICACAAGGAGGCTTATGTTAGCAAGCCAAAGAAGCTTCTCACCTTGCCCATTGC 1508
                                                                                                                                                                                           TTATGCAAAATCTCTTGTGCCCCCTAATAGAACT-TCCTCTCCACTAGCAAAGACATGAA 1567
                                                                                                                                                                                                                       1514 TIATGCAAATCTCTTGTGCCCCCTACAAGAACTCTTGTCACCTCTAGCTAAGGCATAGA 1573
                                                                                                                                                                                                                                         TGAAGTAGTTGAGTCAATGAGTATTATACACTA----AAGAAACTCAGGTACTTGTAAAT 1623
                                                                                                                                                                                                                                                     GAGATAICTIT------IGCTAAATGTGTATCAAAAGTAGATTGT-AAATICAATA 1675
                                                                                                                                                                                                                                                                                Phytoene synthase; transgenic plant; enhanced carotenoid synthesis; ultra violet absorber; food colour; ss.
1094 TATTGCACCTGATTCAAAGGCAACAACAGAGGGGTATATAATGCAGCTTTGGCTTTAGG
                                                       1154 AATCGCAAATCAACTAACGAACATACTCAGAGATGTTGGAGAAGATGCAGAAGAGGGAAG
                                                                                                                               ATTCTTTGATGAGTCAGAAAGGTGTCACAGAACTGGACTCTGCTAGTAGATGGCCTGT
                                               GCTTGCAAATCAACTAACCAATATACTCAGAGATGTAGGAGAAGATGCCAGAAGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                    Phytoene synthase coding sequence from N. tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
363.,1595
/*tag= a
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                                                                                                                                                                                                                                                                                                      1694 TAACAATCTCTAG 1706
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                                                                                                                                                                                                                                                                                                                                             AAV03881 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Length 1814;
                                                                                                                                                                                                                                                                      DNA encoding tobacco phytoene synthase polypeptides - useful producing recombinant polypeptides or transgenic plants
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                                                                                                                                       Hellmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1814 BP; 577 A; 281 C; 441 G; 515 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 49.4%; Score 853.4; DB 19; Best Local Similarity 76.5%; Pred. No. 5.2e-233; Matches 1223; Conservative 0; Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TACAAGTATTGGTTTTTGATAAAATAGGCTGAGGTGAGAAGG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the pharmaceutical and cosmetics industries.
                                                                                                                                     Grill
                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 33-36; 25pp; English.
                                                                                                                                     WP,
                                                                                                                                     Fitzmaurice
DELLA-CIOPPA G R
FITZMAURICE W P.
GRILL L K.
                                              GRILL L K.
HELLMANN G M.
                                                                                            KUMAGAI M H.
                                                                                                                                                                                                      WPI; 1998-086196/08.
P-PSDB; AAW41060.
                                                                                                                                   Della-Cloppa GR,
Kumagai MH;
  (DELL/) I
(FITZ/) E
(GRIL/) (HELL/) H
(KUMA/) H
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us-09-847-081b-1.rng

tomato; TOM5; probe; hybridisation; polymerase chain reaction; PCR antisense; transgenic plant; crop improvement; carotenoid; vector;

Cucumis melo WO9602650-A2

phytoene-synthase; ripening; cDNA library; TOM5; probe; hybridisation; polymerase cha

Melon phytoene-synthase gene.

melon;

(first entry)

13-APR-1996

AAQ99323;

fruit; MEL5;

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Turner

Taylor J,

Karvouni 2,

John I,

Grierson D,

I.O.

(ZENE) ZENECA

22-SEP-1994; 18-JUL-1994; 06-JUL-1995;

95WO-GB01603 94GB-0019081 94GB-0014505

01-FEB-1996

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence encodes melon phytoene-synthase (MEL5 gene), and is almost full-length. The sequence has been isolated as a cDNA clone from a ripening-related cDNA library derived from climacteric melon fruit, using the tomato phytoene-synthase cDNA (TOM5) as a heterologous probe. The MEL5 gene 5'-end has also been isolated by polymerase chain reaction and sequenced. The DNA may be used in sense or antisense constructs to modify gene expression in plants. The carotenoid content and related characteristics of plant parts (particularly fruit) may be modified in this way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGTCTTTGTATCATCCAGGTTCCTAGCTCGAGATAGGAATTTGATGTGGAATGGGAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                               New isolated DNA encoding melon phytoene synthase transform plants to modify carotenoid content and characteristics in plant parts, partic fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 49.1%; Score 847.6; DB 17 Best Local Similarity 77.6%; Pred. No. 2.2e-231; Matches 1136; Conservative 0; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 15-16; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-105912/11.
                                                                                                                                                                                                                                                                                                                                                           Watson C;
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AAQ99323 standard; cDNA; 1591

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· A	1300	CAGAATTGAGCTCAGCTAGATTCCCTGTATGGGCATCTTTGGTCTTGTACGCAAAA	ପୁ	113
οy	1418	TATTGGACGAGATTGAAGCCAACGACTACAACATCACAAGGAGGGCTTATGTTAGCA 147	ογ	218
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8 TGATAAAATAGGCTGAGGTGAGAAGGTAACATAAAGGAAAGACAAAAACTTGGGAATTGT 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        construct to modify synthesis of plant carotenoid(s) -
prises sequence homologous to gene of clone pTOM5 preceded by
nt promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 48.6%; Score 840.4; DB 12; Length 1646; ocal Similarity 74.3%; Pred. No. 2.5e-229; s 1221; Conservative 0; Mismatches 331; Indels 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lence 1646 BP; 529 A; 249 C; 387 G; 481 T; 0 other;
                                                                                                                                                                                                                                                                                                                                        ening; lycopene; transgenic tomato; ss.
                                                                                                                                                                                                                                                                                                                                                                                opersicon esculentum var. Ailsa Craig.
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8 GAACTTCCTCTCCACTAGCAAAGA 1561
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                                                                                                                                                         12495 standard; cDNA; 1646 BP.
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This sequence encodes the phytoene synthetase from Nicotiana benthamiana. The phytoene synthetase coding sequence represents a cDNA of the invention. The isolated nucleic acid molecules are used for producing recombinant polypeptides or transgenic plants with enhanced ability to synthesise carotenoids. Phytoene has been used as a ultra violet absorber.
                                                                                                                                                                                                                                               1648
plant; enhanced carotenoid synthesis;
                                                                                                                                                                                                                                                                                                                                                            AGCCAAAG-AAGCTTCTCACCTTGCCCATTGCTTATGCAAAATCTCTTGTGCCCCCTAAT
                                                                                       AATGTACATTAGAAGAAAAAAGGAAGAAGAAATGTTGTTGTTTGATATAAATGTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hellmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phytoene synthase coding sequence from N. benthamiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytoene synthase; transgenic plant; er
ultra violet absorber; food colour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1..1242
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                                                                                                                                                                                                                                                                                                                                                                                                                          ACACTCATCAAACCCTCAAGTGAG 1728
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Kumagai MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV03879 standard; cDNA; 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 21-26; 25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0579667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotiana benthamiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRILL L K.
HELLMANN G M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELLA-CIOPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GRIL/) GRILL L K.
(HELL/) HELLMANN G M
(KUMA/) KUMAGAI M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-086196/08.
P-PSDB; AAW41058.
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(FITZ/)
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Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone
                                                                                                                                                                                                                                                                                                                                                        Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a phytoene synthase polypeptide, which
   940 ACTGGAAAAGTGACTGATAAATGGAGAAGCTTTATGAAGAAGCAATTCCAGAGGGCAAGA
                                                                                            GCTGGAAGAGTGACTGATAAGTGGAGGAACTTTATGAAGAAACAAATTCAGAGGGCGAGG
                                                                                                                         GTGTTAACAGCGCTGCTGTTGTATCGCAAGATATTGGACGAGATTGAAGCCAACGACTAC
                                                                                                                                                               AACAACTTCACAAGGAGGGCTTATGTTAGCAAGCCAAAGAAGCTTCTCACCTTGCCCATT
                                                                                 AAATTCTTTGATGAGTGAGAAAGGTGTCACAGAACTGGACTCTGCTAGTAGATGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Logusch
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "phytoene synthase"
/transl_except* (pos: 1027..1029,
/transl_except* (pos: 1057..1059,
                                                                                                                                                                                                      cDNA encoding a phytoene synthase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
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1..1239
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/product=
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P-PSDB; AAY84101.
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07-JUN-1999;
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Piller KJ,
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                                                                       Gaps
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                                                 Score 811.2; DB 19; Length 1316;
Pred. No. 4.9e-221;
0; Mismatches 173; Indels 84;
   animal
                            Sequence 1316 BP; 403 A; 221 C; 342 G; 350 T; 0 other;
   colours,
                                                                                                                                                                                                                                GGTTCTGTAA---------
  food
 lds have been used as food
and cosmetics industries
 other carotenoids have been
                                                 46.9%;
80.2%;
                                                                     Conservative
and other carotenor
the pharmaceutical
                                                           Similarity
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Matches 1039;
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is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels and be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway sequence, diverts rhe methods uses copally diphosphate synthase, 3beta-hydroxylase, 7-oxidase, phytoenel synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of glibberellin biosynthetic pathway and restoration of normal seed
                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                         germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
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                                                                                                                                                                                                                                                                                                                             250 ATGTCTGTTGCTTTGTTGTGGGTTGTTTCTCCCACTTCCGAGGTCTCGAATGGGACAGGA 309
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                          1 AIGTCIGITGCCTIGITATGGGTTGTTCTC---CTTGTGACGTCTCAAATGGGACAAGT 57
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                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                    DB 21; Length 1239;
                                                                                                                                                                                                                                                               Score 806.4; DB 21; Length
Pred. No. 1.1e-219;
0; Mismatches 206; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1239 BP; 376 A; 208 C; 316 G; 339 T; 0 other;
                                                                                                                                                                                                                                                                 46.78;
78.88;
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                                                                                                                                                                                                                                                                               1390 TTAACAGCGCTGCTGTTGTATCGCAAGATATTGGACGAGATTGAAGCCAACGACTACAAC 1449
                                                                                                                                                                                                                                                                                                                             AACTICACAAGGAGGCTIAIGIIAGCAAGCCAAAGAAGCTICTCACCTIGCCCATIGCT 1509
                                                                                                                                        GTATACTTGCCTCAAGATGAATTAGCACAGGCAGGGCTCTCCGACGAAGACATATTTGCT 1269
                                                                                                       829 ATCGCAAATCAATTAACTAACATACTCAGAGATGTTGGAGAAGATGCCAGAAGAGGGAAGA 888
                                                                                                                                                                                                                                               1069 IGGGCATCTTTGGTCTTGTACCGCAAAATACTAGATGAGATTGAAGCCAATGACTACAAC
            1090 ATTGCACCTGAATCAAAGGCAACAGAGAGTGTATATAATGCTGCTTTGGCTTTAGGG
                                                                                           1150 CTIGCAAATCAACTAACCAATATACTCAGAGATGTAGGAGAAGATGCCAGAAGAAGAAGA
TATCTCTATTGTTACTATGTTGCTGGTACTGTAGGATTGATGAGTGTTCCAGTTATGGGT
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The present sequence encodes phytoene synthase 4. It was isolated from a cDNA library prepared from mRNA extracted from the petals of Gentiana lutea. The nucleic acid sequence was amplified from the library using PCR primers AAV16952-53. The phytoene synthase gene is useful for breeding plants with variable flower colours.
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                                                                                                                                                                                                     TGGGACAGGATTGTTGGATTCAGTCCGAGAAGGAAACCGCGTCTTTGTATCATCCAGGTT 359
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                                                                                                                               30;
                                                                                                     DB 19; Length 2868;
                                                                                                  Score 692.4; DB 19; Length
Pred. No. 6e-187;
0; Mismatches 311; Indels
                                                                            Sequence 2868 BP; 887 A; 499 C; 648 G; 833 T; 1 other;
                                                                                                                                                                                                                              TGGCAATGTTTCTTGGAGCCAATTCGAGAAAGTTACCATTTTTCG---
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73.6%;
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Matches 949; Conservative
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                         GAGGGCGAGGAAATTCTTTGATGAGTCAGAAAGGTGTCACAGAACTGGACTCTGC-TA
                                                                                                                                       GTAGATGGCCTGTGTTAAC - - AGCGCTGCTGTTGTATCGCAAGATATTGGACGAGTTGA
                                                                                                                                                                           AGCCAACGACTACAACGTTCACAAGGAGGGCTTATGTTAGCAAGCCAAAGAAGCTTCT
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                                                                                                                                                                                                                                                                                                                                                            colour;
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Length 1921;

DB 19;

Score 678.4;

39.38;

Match

Query

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TGAGGACATTTTTGCTGGAAAAGTTACAGACAAATGGAGGATTTTTATGAAGAAGCAAAT
                            TAGTAGATGCCCTGTTTAACAGCGCTGCTGTTGTATCGCAAGATATTGGACGAGATTGA
                                                            TCAGAGGGCGAGGAAATTCTTTGATGAGTCAGAGAAAGGTGTCACAGAACTGGACTCTGC
                                                                                                                                                                                                                                                  colour;
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Pred. No. 9.8e-181;
0; Mismatches 331;
                                                                                                                                                                                                                                                  variable flower
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                                                         TGGGACAGGATTGTTGGATTCCAGAAGGAAACCGCGTCTTTGTATCATCCAGGTT
                                                                         462 TGGCAATGTTTTCTTGGAGCCAATTCGAGAAAGTTACCATTTTTCG------
                                                                                          CCTAGCTCGAGATAGGAATTTGATGTGGAATGGGAGAATCAAGAAAGGTGGGAGACAAAG
                                                                                                                           GIGGAATITIGGCICTITAATIGCICATCCAAGATATICATGCTIGGGIGGATCAAGAAC
                                                                                                                                                           480 TGAAA----AGGGAAGCACTTTCTCTGTACAGTCCAGT--TTGGTGGCTAGCCCAGCTGG
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         30;
         Indels
Pred. No. 4.9e-183;
0; Mismatches 326;
1larity 72.4%;
Conservative
Similarity
         934;
Best Local
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'n The present sequence encodes phytoene synthase 1. It was isolated from a cDNA library prepared from mRNA extracted from the perals of Gentiana lutea. The nucleic acid sequence was amplified from the library using PCR primers AAV1692-53. The phytoene synthase gene is useful for breeding plants with variable flower colours. TGGACAGGATTGTTGGATTCAGTCCGAGAAGGAAACCGCGTCTTTGTATCATCCAGGTT 359 576 TICTGITAACAIGICTATITGIACGCIAIGGGITGITICGCCGAGITCTGAAGTTITGAG 635 Gaps 30; 2085; variable Length Indels Sequence 2085 BP; 654 A; 320 C; 479 G; 632 T; 0 other; breeding plant of TTTCATGAGCATGTCTGTTGCTTGTTGTGGGTTGTTTCTCCCACT 19;

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llarity 72.6%; Pred. No. 6.8e-176;
Conservative 0; Mismatches 321;
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Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                              Arabidopsis thallana DNA fragment SEQ ID NO: 9067
                   ВР
                 AAC35120 standard; DNA; 1703
                                                                                           (first entry)
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990S-0139817.
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DB 21; Length 1703; Score 578.6; DB 21; Length Pred. No. 1.5e-154; 0; Mismatches 269; Indels 33.5%; Ouery Match Best Local Similarity 73.4 Matches 769; Conservative

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653

595 ACAGCTAAGGTCTTCTTTTTATGATCTGAAGAAACCACAAGATGTTGTTCTTCC 654

603 GCAGCTGAG---ATCTACCGATGATTTAGAAGTGAAG-----CCGGATATTGTTGTTCC

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protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; s
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              TGCTAAGACGTTTTATCTTGGAACTTTGCTTATGACACCCGAAAGGCGAAAGGCGATTTG
                                                                       GGCAATATATGTGTGGTGCAGGAGAACGGATGAGCTTGTTGATGGCCCTAATGCATCCCA
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                                                                                                                GCCATTIGATAIGCITGAIGCIGCTITAICCGATACIGICTCCAGATTICCIGITGAIAT
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                                                                                                                                                                                                                 1074 TGTTCCAGTTATGGGTATTGCACCTGAATCAAAGGCAACAACAAGAGGTGTATATAATGC
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281; Indels

Score 578 4; DB 21 Pred. No. 1.6e-154; 0; Mismatches 281;

33.5%; ilarity 72.5%; Conservative

DB 21; Length 1566;

533 388 593

474 AAGAACIGAAAAGGGAAGCACTIICICIGIACAGICCAGIIIGGIGGCIAGCCCAGCIGG

534 389 594

AGTGAAGAGGCAGCTGAGATCTAC-------CGATGATTTAGAAGTGAAGCCGGATAT

645 509

448

644

704

628

269

705 TGCAGAGTATGCAAAGACATTTTACTTAGGAACCAAGCTAATGACCCCAGAGAGAAGAAG

765 AGCTATCTGGGCAATATATGTGTGTGCAGGAGAACGGATGAGCTTGTTGATGGCCCTAA

688 824

99US-0152363. 99US-0153070. 99US-0153758. 99US-0154018. 990S-0154039 990S-0154139 990S-0155486 990S-015559 990S-015559 990S-01559 990S-015786 990S-015786 990S-0158029 990S-0158029 990S-0159294 990S-0159294 990S-015938 990S-015938 990S-015938 990S-015938 990S-015938 990S-015938 990S-015938 990S-015938 99US-0160815. 99US-0160980. 99US-0160981. 99US-0160989. 99US-0161992. 99US-0161993. 99US-0162142. 99US-0161404 99US-0161405 99US-0161406 990S-0161359 990S-0161360 990S-0161361 990S-0161920 13-SEP-1999; 15-SEP-1999; 16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 28-SEP-1999; 29-SEP-1999; 04-OCT-1999; 05-OCT-1999; -OCT-1999; 3-OCT-1999; 4-OCT-1999; 4-OCT-1999; 4-OCT-1999; 1-OCT-1999; 1-OCT-1999; 1-OCT-1999; 1-OCT-1999; 1-OCT-1999; 25-OCT-1999 25-OCT-1999 08-OCT-1999 -OCT-1999 2-OCT-1999 3-0CT-1999 28-OCT-1999 -OCT-1999 26-OCT-1999 -OCT-1995 -0CT-1 2-0CT-1

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                                                                 945 TGTTGATATTCAGCCATTCAGAGATATGATGAAGGAATGCGTATGGACTTGTGGAAATC
                                                                                                                         869 GAGATACCAGAACTICGATGATCTATCTTACTGCTACTACGTCGCTGGAACCGTCGG
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